

-1696 TGT^tTGGCAT^tAAGTIC
 -1680 ATAGATTTATAATTGTAAATGGAATCACACCAAAATGCAAAT^tAGAAAGAGAGGCCACTT^tGCTCACCCAGTCACGHTC
 -1600 CCATGTAACCATAAGAACGTTGGGTCCTGTCTTAGATCACAAGTCTTGCTCTAGAACAGGCTAGUCCACACCA
 -1520 GGCCNAGTGCAGGACCCATGGCCCTTTTAAAGTCAGACTCCCTCTGTAACAGCAATATCCCACAACT^tGTCACAA
 -1440 CNT^tGGTGCCTCCUGAAGGGCTACAGAACTATTGTATAGCAAAATGTCTATGACUTACACAGAACAGAACAAAT
 -1360 AAAAATTAAATAATTAAATTTAAATGTCTTGAAATGTACCAATTATTACATTTTACATTTGGGCTCAVAAAAT^tGTTATTACAC
 -1280 TTAGGAATGCAATACAAATTGAAAGATCAGATTTCCTCCCT^tTGTGAAATTCTCAAGTATGTCATGACUTACCAAGAA
 -1200 ATCATAGCCAGTCATTAATTCAGTGAGTFACTCATTAACAGAACAGAACCACTACTCTTGGAGAATGGCTAGGCTTGCTTC
 -1120 CCTTCAACTCAGGATATAACACTGCTTCAACTGCTTCTCAGTAACTTGTCAACTTGTCAACTAAT^tAGAACGCTGTGCTTAACAA
 -1040 TTTTAIGGTTGACTCTCCCTGGCTCAGGGTTCAGGTTCCCTAGAACAGAGAGETCCCCAAATTCCGGCTGTGCTGTCGGC
 -960 CTANGCTCAGCCAGATCAGCAGGGCATAGATTCTCATAGGAGCTGGACGCCATTGTCAGCTGCGTATGT
 -880 GGGGGATCCAGATTTGGCACTCTTTATGAGAACTAACTAATGCTGTATGATCTCATCTGACAGAACAAATT^tCATTCCTG
 -800 AAACCAATCCCCAACAAATCCATAAAATACTGTTCCACAAAAAATGATCCCTGGCCAMAAATGTTAGAGACCACTCC
 -720 CCTAAAAACTCTCTCTTAGCTCTAGCTCTACCTCTGTAACTACTTCATCTCATCTGACATTGAGGCCCATCTTTCCTCATG
 -640 GATGCTCTCATTTCTTATTAGGGAGGCATTTTTATTATTTTTGTGTTTCTTCTGAGAGATCTCTGCTCTGTC
 -560 CAAGGCTGGAGTGCACTGGCGCATCTGGCTCACTGCAAGGCTCCGGGETTCAGGCAATTCTCTGUCUCCAGC
 -480 TCCCCAAGTTGGGACTACAGGGCCCGCAATTAGCCCGCTTAATTTTGTAGAGACGAGGTTTTCACCG

-400 TGGTAGCCAGGATGGCTCGATECTCCGTGACCTCGU'UCGCCUGCU'U'GGCTCCCAAAGTGGTGGGA'TACAGGGCIG
 -320 AGACCGCGCCGGCGCATTTGGTATGTCATAATGTCCTAGAACCTAGGACAGTCCCCTGTAACCAGTAGAGACCTA

 -240 TGTAAATGTCGTTATTCATAATAATACATGAAATTAAAGAGTGAGAGTGAGGATTGTGAAAGTGTGACTGAAAGAAA
 -160 TACTCA GTGATTCTAAGGGATGGGAAAGAACGGTTGGGCTAGAGGTGTGCTCAGGAAACTATTAATAAGACGTCCGC

 -80 AGGAAGGGATGACGAAAGTGTGAGTTAATGAGGAAGGAAATAAGAATAAAATTTGGTGTGAAAGTGTGAGGAA

 1 ● ATGATGCCGTGTCAGAGAGCAAGGCTCTGTCGCTTGTGCTTAATTTGGTGTGCTGTCGTCGTCGTCGTCGTC

 2 / 21 -24 -20 -10 +1

 +81 TTTGCCCTCCGAGGAGCCTGTTGGAAAGAG ATG GTC ATG GGC CTC GGC GTC GTC GTC GTC

 +144 Val Leu Gly Leu Thr Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 +144 GTG CTG GGT CTG GGT CTG ACC CCA CCG ACC CTC GCT CAG GAT AAC TCC AGG TAC ACA CAC

 10 phe Leu Thr Gln His Tyr Asp Ala Lys pro Gln Gly Arg Asp Asp Arg Tyr Cys Glu Ser
 +204 TRC CTG ACC CAG CAC TAT GAT GCC AAA CCA CAG GGC CGG GAT GAC AGA TAC TGT GAA AGC

Fig. 1B

		40						
3.0	Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His Gly							
+2.64	ATC ATG AGG AGA CGG GGC CTG ACC TCA CCC TGC AAA GAC ATC AAC ACA TTT ATT CAT GGC							
		50						
	Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn Lys Asn Gly Asn Pro Ile Arg Glu Asn							
+3.24	AAC AAG CGC AGC ATC AAG GCG ATC TGT GAA AAC AAC TAA GAT GCA AAC CCT CAC AGA GAA AAC							
		60						
	Ileu Arg Ile Ser Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro							
+3.84	C ^{TA} AGA ATA AGC TAA TCT TCT CAG GTC ACC ACT TGC AAC GTC AGG CTA CAT GGA GGT							
		70						
	Ileu Arg Ile Ser Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro							
+4.44	TGG CCT CCA TGC CAG TAC CGA GCC ACA GCG GGG TCC AGA AAC GTT GTC GCT TGT GAA							
		80						
		90						
	Terp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Ala Cys Glu							
+4.44	TGG CCT CCA TGC CAG TAC CGA GCC ACA GCG GGG TCC AGA AAC GTT GTC GCT TGT GAA							
		100						
		120						
	Asn Gly Leu Pro Val His Leu Asp Glu Ser Ile Phe Arg Arg Pro Stop							
+5.04	AAT GGC TTA CCT GTC CAC TTG GAT CAG TCA ATT TTC CGT CGT CCG TAA							
		130						
	CCAGGGCCCCCTGGTCAAGTGCTGGCTCTGGCTCTGGCTCTGGACCTTGTGTTCTGTTGACAAC							
+6.12	CCCAGAACAGTGGTGGCAACATTGTGCCAGTATCATGAGAAATGCGCTTCTGATTCTGGCATATTCGATCTTGTGTTTCCCC							
		140						
+6.92	ATGTTTAATTAATAAAATGTCCTGTCATAGGATATCAAGAAATGCGCTTCTGATTCTGGCATATTCGATCTTGTGTTTCCCC							

Fig. 1C

+214.2 TAGAAAGTGGTTGCCAATAAATTAAGTTATAAGTTCGCGAGT'T'CACTGCCTTGTTGAAACATATAATTAT'ATGTTGGGTCAGTA
+223.2 TTCCCTATATGGGGTTTCTCCCTGCCTGGTATTGCCCTGAAATGGCCAAAGGCCGTGGCTCCCCAATGCTCAGGTATA
+23.02 GAAACATTTGTCAGGTAACCTAGAGAGGCCAGCTCACTGAGAGTATTCAAAATTAGGAATGGGATGGTTGAGAAGTAGGT
+23.82 AGCTGGTATGTGCTTAGCACAAAGAACTCTCTCCCTGGGT'AGCTGTTCAAAACTGAAACACTGTCATTCCTTAAG
+246.2 AAATTAAGGAAAGTATTCMAACCTCTGTGACTAGAAAATTTGCCATATTAACCAAAATTCAGGAATTCAGGAATAAC
+254.2 AGAAAGTCCCAGTTCTGTGAAACTATTGGCCCTTTCTCAACTTCCAGTGCTCCCTCCAGTGTATTGAGGTGGGCA
+262.2 MAGTTACTCAAGATCATCGCTGCACACTCAAGGGCTTGTAGGGCAGTGAAGGCNTGGACCATTAATTTATATCACA
+270.2 GCATYAGCTGTGAAACACATCTTCACATCTCCTGGACMTTATGATCGCATWGTPTUCLUTGGTGTICAGG
+278.2 GAAAATGCTGTGTTCTAGGAATAATCACATGGCAGTGGGATGGAGTGTTCCCTGACCTGGGATGGHTACTGCACTTGACC
+286.2 AAGCTTCTCTAGTCCTTGGCTGGGCTCTGGTCTATCACAAACCAAGCTGTTAAATAAAAACGTCAAGTCAC
+294.2 AGGGCAAGGTCAATTATCCTGCGTGAATCAATTGAG

Fig. 1E

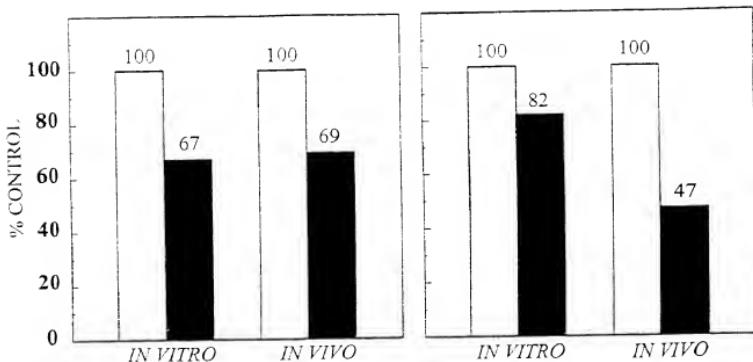


Fig. 2A

Fig. 2B

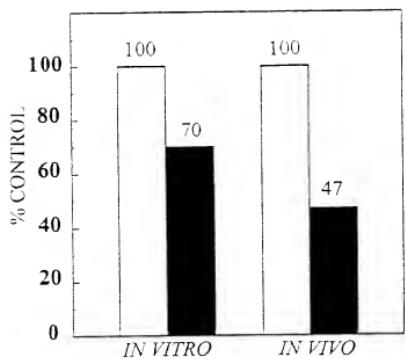


Fig. 3A

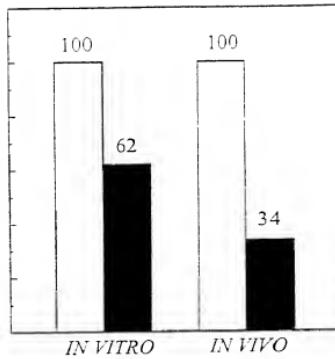


Fig. 3B

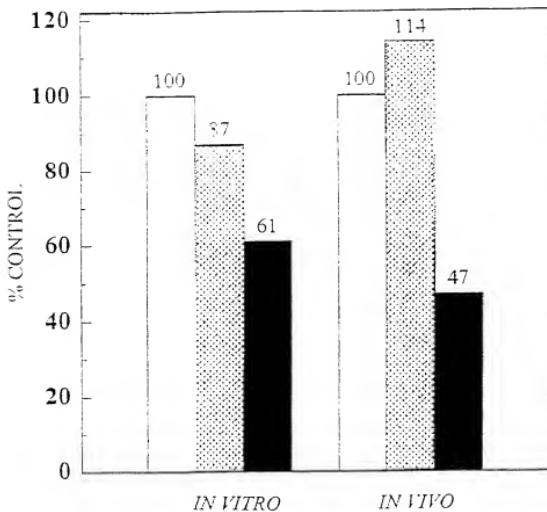


Fig. 4

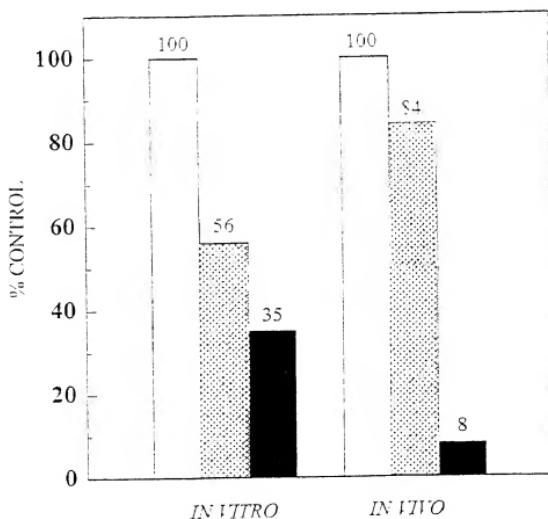


Fig. 5

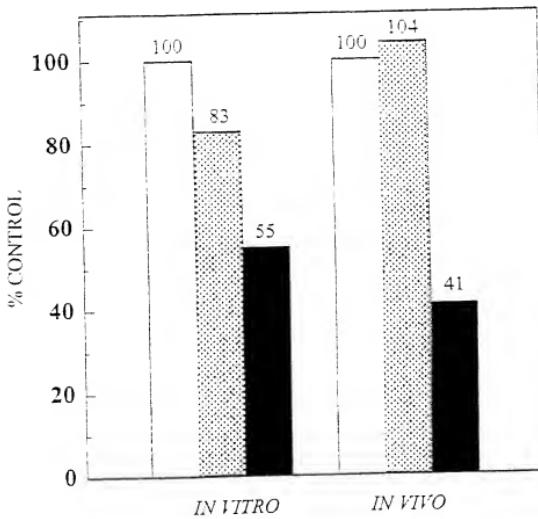


Fig. 6

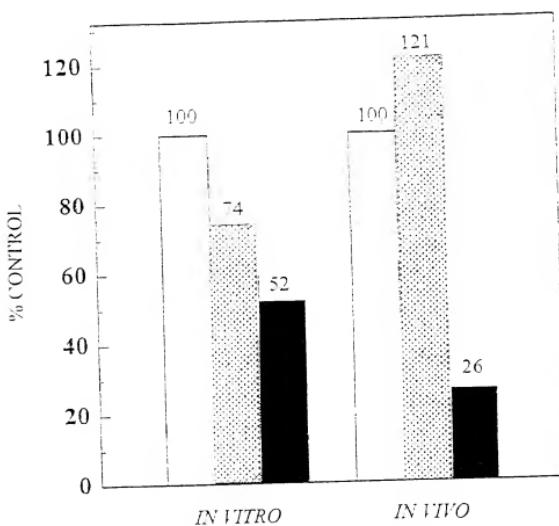


Fig. 7

FIG. 8

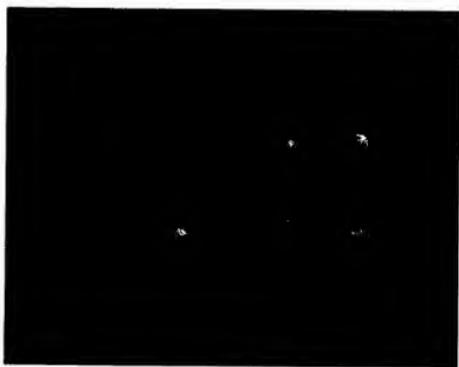


FIG. 9

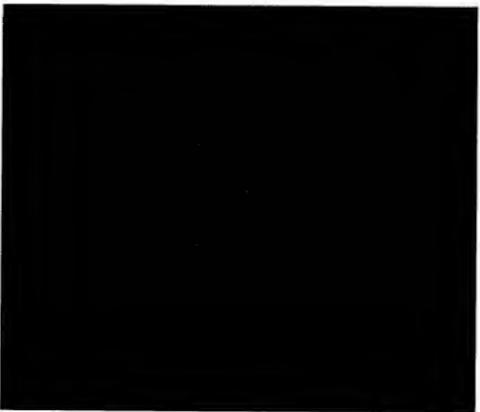


FIG. 10

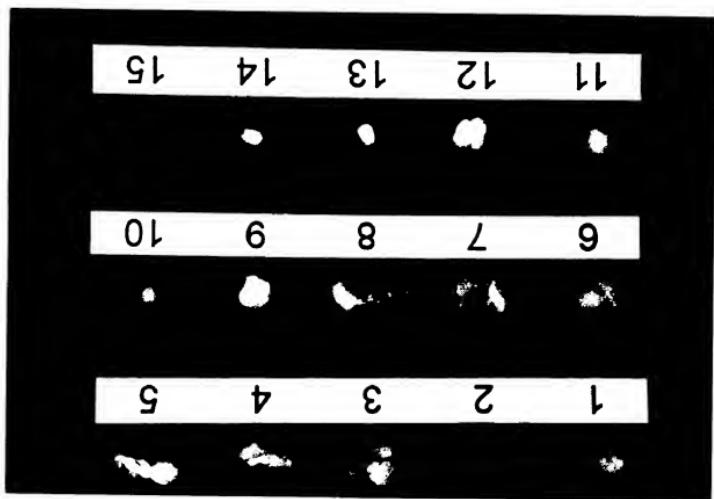


FIG. 11

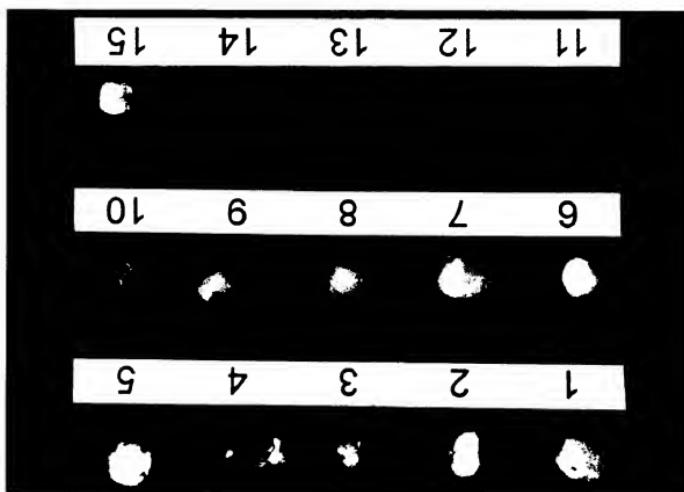


FIG. 12

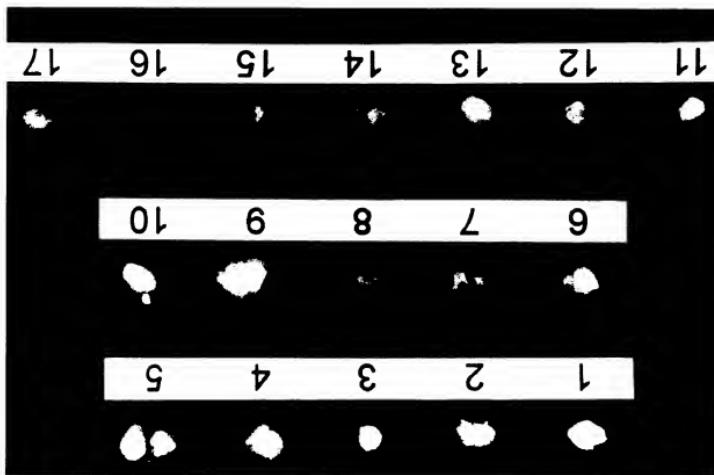


FIG. 13

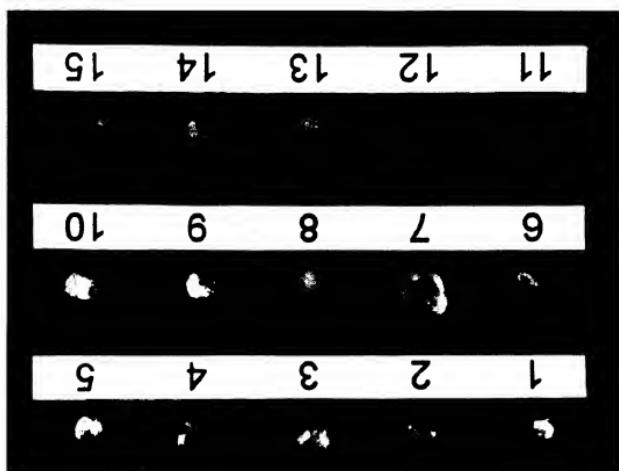
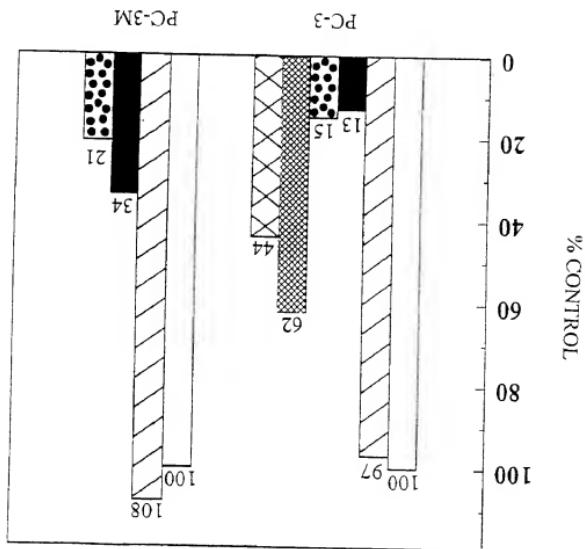


Fig. 14



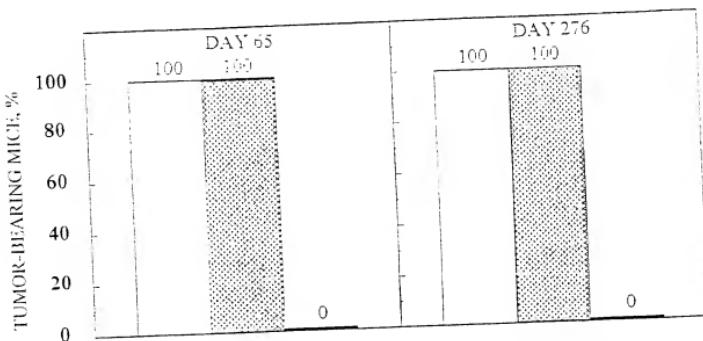


Fig. 15A

Fig. 15B

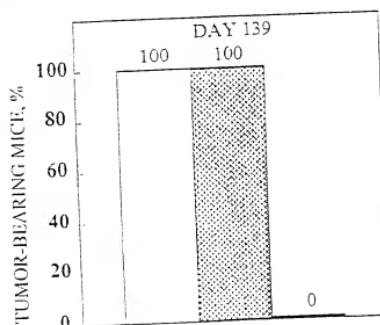


Fig. 15C

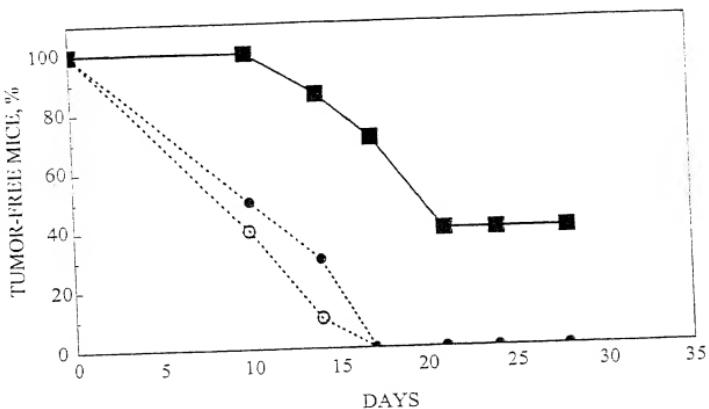


Fig. 16

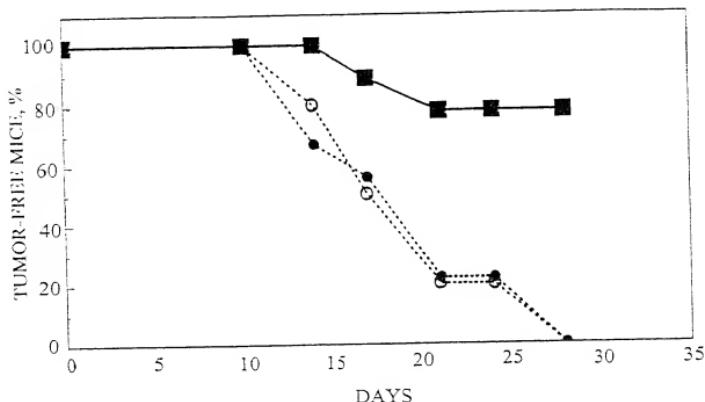


Fig. 17